WHAT IS CLAIMED IS:

1. A method of mapping the location of a post-translational modification of a post-translationally modified peptide, said method comprising:

(a) contacting said peptide with a chemical modification reagent that converts a post-translationally modified amino acid residue of said peptide into a substrate for a peptidase, thereby producing a chemically modified peptide comprising a chemically modified amino acid residue;

(b) contacting said chemically modified peptide with said peptidase under conditions appropriate to degrade said chemically modified peptide, thereby producing a degraded chemically modified peptide; and

(c) querying said degraded chemically modified peptide to ascertain said location of said post-translational modification.

2. The method of claim 1, further comprising:

(d) prior to step (a), contacting a substrate amino acid of said peptide that is a natural substrate for said peptidase with a blocking agent thereby converting said substrate amino acid into a side-chain protected amino acid that is not a substrate for said peptidase.

3. The method of claim 2, wherein said substrate amino acid is a lysine, wherein said blocking agent converts said lysine into a side-chain protected lysine selected from the group consisting of a carbamate, an amide, an N-sulfonyl, an N-sulfenyl, an N-nitro, an N-nitroso, an N-oxide, an imine, an N-alkyl amine, an N-aryl amine, an N-phosphinyl, an N-phosphoryl, and an enamine .

4. The method of claim 2, wherein said side chain protected lysine is selected from the group consisting of Lys(Aloc), Lys(Ac), Lys(Boc), Lys(biotinyl), Lys(2-bromo-Z), Lys(2-chloro-Z), Lys(Dnp), Lys(Fmoc), Lys(For), $Lys(Me)_2$, Lys(nicatinoyl), Lys(Tfa), Lys(Tos), Lys(Z), Lys(Z)(isopropyl), Lys(Boc)(isopropyl), Lys(dansyl), Lys(Dde), $Lys(Me)_3$, Lys(Mtt), Lys(palitoyl_, Lys(TNM), Lys(acetimidoyl), Lys(2,4,-dichloro-Z), Lys(Me), Lys(p-nitro-Z), Lys(5/6 FAM), Lys(pyrenebutyryl), and Lys(guanidinyl).

5. The method of claim 1, wherein said substrate amino acid is aspartic acid, wherein said blocking agent converts said aspartic acid into a side-chain protected aspartic acid selected from an ester, an amide, an oxalose, an oxazolines, a stannyl ester, and an hydrazide.

6. The method of claim 1, wherein side chain protected aspartic acid is selected from the group consisting of Asp(OBzl), Asp(OcHex), Asp(OtBu), Asp(OMpe), Asp(Ofm), Asp(Osu), Asp(2-phenyisopropyl ester), and Asp(ONp).

7. The method of claim 1, wherein said peptidase is selected from the group consisting of a serine endopeptidase, a metalloendopeptidase, a cysteine endopeptidase, and an aspartic endopeptidase.

8. The method of claim 1, wherein said peptidase is a lysine-specific peptidase.

9. The method of claim 8, wherein said lysine-specific peptidase is selected from the group consisting of endoproteinase Lys-C, lysyl endopeptidase, trypsin, plasma kallikrein, oligopeptidase B, tryptase, plasmin, acrosin, granzyme A, yapsin 1, peptidyl-Lys metalloendopeptidase, and magnolsyin.

10. The method of claim 8, wherein said lysine-specific peptidase is selected from the group consisting of endoproteinase Lys-C, lysyl endopeptidase and trypsin.

11. The method of claim 1, wherein said peptidase is an aspartate-specific peptidase.

12. The method of claim 11, wherein said aspartate-specific peptidase is selected from peptidyl-aspartate metalloendopeptidase and nepenthesin.

13. The method of claim 1, wherein said querying comprises mass spectrographic detection of said chemically modified amino acid residue of said degraded chemically modified peptide.

14. The method according to claim 1, further comprising:

(e) prior to step (a), contacting said peptide with an elimination reagent that causes the elimination of a post-translationally added substituent of said post-translationally modified amino acid residue.

15. The method of claim 14, wherein said post-translationally modified amino acid residue is selected from the group consisting of a post-translationally modified serine and a post-translationally modified threonine.

16. The method of claim 14, wherein said post-translationally modified amino acid residue is a phosphorylated amino acid residue.

17. The method according to claim 14, wherein said elimination is a β-elimination giving rise to an alkene moiety.

18. The method according to claim 1, wherein said modification reagent reacts with said post-translationally modified amino acid residue via a Michael addition.

19. The method of claim 18, wherein said modification reagent is selected from the group consisting of sodium sulfate and cysteamine.

20. A reactive solid phase material comprising:

(a) a solid support; and

(b) a solid support reactive moiety immobilized on said solid support, wherein said solid support reactive moiety is reactive towards a synthetically modified amino acid residue of a post-translationally modified peptide, said synthetically modified amino acid residue produced by elimination a post-translationally added substituent of said post-translationally modified peptide.

21. The material according to claim 20, wherein said synthetically modified amino acid residue comprises an alkene moiety.

22. A method of immobilizing a post-translationally modified peptide comprising a post-translationally modified amino acid, said method comprising:

(i) contacting said peptide with an elimination reagent that causes the elimination of a post-translationally added substituent of said post-translationally modified amino acid residue thereby producing a synthetically modified amino acid;

(ii) reacting said synthetically modified amino acid with a reactive solid phase material thereby immobilizing said post-translationally modified peptide, said reactive solid phase material comprising:

(a) a solid support; and

(b) a solid support reactive moiety immobilized on said solid support, wherein said solid support reactive moiety is reactive towards said synthetically modified amino acid residue.